Amendments to the Claims

Please cancel Claims 27-29 and 31-41.

Please amend Claim 30.

The Claim Listing below will replace all prior versions of the claims in the application:

Claim Listing

What is claimed is:

1. (Withdrawn) Isolated nucleic acid encoding a mammalian SCA2 polypeptide.

2. (Withdrawn) The isolated nucleic acid of Claim 1 which is DNA.

3. (Withdrawn) The isolated nucleic acid of Claim 2, wherein the DNA is cDNA.

4. (Withdrawn) The isolated nucleic acid of Claim 2 which encodes at least about 10 contiguous amino acids set forth in SEQ ID NO: 3 or at least about 10 contiguous amino acids set forth in SEQ ID NO:5.

5. (Withdrawn) The isolated nucleic acid of Claim 2 which hybridizes under high stringency conditions to nucleotides 1 - 516 of SEQ ID NO:1, nucleotides 163-4098 of SEQ ID NO:2 or SEQ ID NO:4.

6. (Withdrawn) The isolated nucleic acid of Claim 2, which has substantially the same nucleotide sequence as nucleotides 1 - 516 of SEQ ID NO:1, nucleotides 163-4098 of SEQ ID NO:2 or SEQ ID NO:4.

7. (Withdrawn) A vector comprising the isolated nucleic acid of Claim 2.

8. (Withdrawn) The isolated nucleic acid of Claim 2 which hybridizes under high stringency conditions to nucleotides 163-4098 of SEQ ID NO:2.

9. (Withdrawn) The isolated nucleic acid of Claim 2, which has substantially the same nucleotide sequence as nucleotides 163-4098 of SEQ ID NO:2.

10. (Withdrawn) An isolated oligonucleotide comprising at least 15 nucleotides capable of specifically hybridizing with a sequence of nucleic acids of the nucleotide sequence set forth in SEQ ID NO:2 or the nucleotide sequence set forth in SEQ ID NO:4.

11. (Withdrawn) The isolated oligonucleotide of Claim 10 which is labeled with a detectable marker.

12. (Withdrawn) The isolated nucleic acid of Claim 2, wherein the DNA has at least 90% homology to the SCA2 coding portion set forth in SEQ ID NO:2.

13. (Withdrawn) The isolated nucleic acid of Claim 1, encoding a mouse SCA2 polypeptide.

14. (Withdrawn) The isolated nucleic acid of Claim 1, which is DNA.

15. (Withdrawn) The isolated nucleic acid of Claim 14, wherein said DNA is cDNA.

16. (Withdrawn) The isolated nucleic acid of Claim 14, which hybridizes under high stringency conditions to the SCA2 coding portion of SEQ ID NO:4.

17. (Withdrawn) The isolated nucleic acid of Claim 14, which has at least 90% homology to the SCA2 coding portion set forth in SEQ ID NO:4.

18. (Withdrawn) A vector comprising the isolated nucleic acid of Claim 14.

19. (Withdrawn) An isolated nucleic acid comprising nucleotides 163-657 of SEQ ID NO:2.

20. (Withdrawn) An isolated nucleic acid comprising nucleotides 724-4098 of SEQ ID NO:2.

21. (Withdrawn) An isolated nucleic acid comprising at least about 15 contiguous nucleotides from nucleotides 163-657 of SEQ ID NO:2, or the nucleotides complementary thereto.

22. (Withdrawn) An isolated nucleic acid consisting of at least about 15 continuous nucleotide from nucleotides 724-4098 of SEQ ID NO:2, or the nucleotides complementary thereto.

23. (Withdrawn) An isolated nucleic acid comprising nucleotides 163-4098 of SEQ ID NO:2.

24. (Withdrawn) An isolated nucleic acid comprising SEQ ID NO:4.

25. (Withdrawn) A single strand DNA primer comprising a nucleic acid sequence derived from the isolated nucleic acid of Claim 1.

26. (Withdrawn) The single strand DNA primer of Claim 25 wherein the nucleic acid comprises the nucleic acid sequence set forth in SEQ ID NO:2 or the nucleic acid sequence set forth in SEQ ID NO:4.

Claims 27.-29. (Canceled).

30. (Currently Amended) A method of diagnosing spinocerebellar ataxia type 2 in a human nucleic acid sample comprising the steps of:

amplifying said nucleic acid sample with a first primer and a second primer by polymerase chain reaction, wherein said first primer hybridizes to a region of nucleotides 303 to 657 of SEQ ID NO:2 and said second primer hybridizes to a region of nucleotides 723 to 890 of SEQ ID NO:2;

obtaining an amplification product of said nucleic acid sample by said polymerase chain reaction; and

measuring a number of CAG repeats in said amplification product by hybridizing a probe to said amplification product, wherein said probe has a sequence comprising greater than 22 CAG repeats,

wherein a normal number of CAG repeats in said nucleic acid sample would be negative for spinocerebellar ataxia type 2.

Claims 31.-41. (Canceled).